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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/259,389DATE: 03/15/1999
TIME: 14:17:32

Input Set: I259389.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

1 <110> APPLICANT: Georgopoulos, Katia
 2 Mogan, Bruce A.
 3 Kelly, Clair

4 <120> TITLE OF INVENTION: THE HELIOS GENE

5 <130> FILE REFERENCE: 10287/043001

6 <140> CURRENT APPLICATION NUMBER: US/09/259,389

7 <141> CURRENT FILING DATE: 1999-02-26

8 <150> EARLIER APPLICATION NUMBER: US 60/076,325

9 <151> EARLIER FILING DATE: 1998-02-27

10 <160> NUMBER OF SEQ ID NOS: 17

11 <170> SOFTWARE: FastSEQ for Windows Version 3.0

12 <210> SEQ ID NO 1

13 <211> LENGTH: 1598

14 <212> TYPE: DNA

15 <213> ORGANISM: Mus musculus

16 <220> FEATURE:

17 <221> NAME/KEY: CDS

18 <222> LOCATION: (1)...(1578)

19 <400> SEQUENCE: 1

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 21 Met Glu Thr Asp Ala Ile Asp Gly Tyr Ile Thr Cys Asp Asn Glu Leu
 22 1 5 10 15
 23 tca ccc gaa ggg gaa cac gcc aat atg gcc att gac ctc acc tca agc 96
 24 Ser Pro Glu Gly Glu His Ala Asn Met Ala Ile Asp Leu Thr Ser Ser
 25 20 25 30
 26 acg ccc aat gga cag cac gcc tcg cca agt cac atg aca agc aca aat 144
 27 Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asn
 28 35 40 45
 29 tct gta aag ctg gaa atg cag agt gat gaa gag tgt gac agg cag ccc 192
 30 Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Gln Pro
 31 50 55 60
 32 ctg agc cgt gag gat gag atc agg ggc cac gat gag ggg agc agc cta 240
 33 Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser Ser Leu
 34 65 70 75 80
 35 gaa gaa ccc cta att gag agc agc gag gtg gcc gac aac agg aaa gtc 288
 36 Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg Lys Val
 37 85 90 95
 38 cag gac ctt caa ggc gag gga gga atc cgg ctt ccg aat ggt aaa ctg 336
 39 Gln Asp Leu Gln Gly Glu Gly Ile Arg Leu Pro Asn Gly Lys Leu
 40 100 105 110
 41 aaa tgt gac gtc tgt ggc atg gtt tgc att ggg ccc aat gtg ctt atg 384
 42 Lys Cys Asp Val Cys Gly Met Val Cys Ile Gly Pro Asn Val Leu Met
 43 115 120 125
 44 gta cat aaa agg agt cac act ggt gag cgg ccc ttc cac tgt aac cag 432

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45	Val His Lys Arg Ser His Thr Gly Glu Arg Pro Phe His Cys Asn Gln			
46	130	135	140	
47	tgc gga gct tct ttt acc cag aag ggc aac ctt ctg aga cac ata aag	480		
48	Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys			
49	145	150	155	160
50	tta cac tct gga gag aag ccc ttc aaa tgt cct ttc tgt agc tat gct	528		
51	Leu His Ser Gly Glu Lys Pro Phe Lys Cys Pro Phe Cys Ser Tyr Ala			
52	165	170	175	
53	tgt aga aga agg gac gct ctc aca gga cac ctc agg acc cat tct gtg	576		
54	Cys Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val			
55	180	185	190	
56	ggt aaa cct cac aag tgt aac tac tgt ggc cga agc tac aag cag cgc	624		
57	Gly Lys Pro His Lys Cys Asn Tyr Cys Gly Arg Ser Tyr Lys Gln Arg			
58	195	200	205	
59	acg tca ctg gag gaa cac aag gaa cgc tgt cac aac tat ctc cag aat	672		
60	Thr Ser Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Gln Asn			
61	210	215	220	
62	gtc agc atg gag gct gcc ggg cag gtc atg agt cac cat gta ccg cct	720		
63	Val Ser Met Glu Ala Ala Gly Gln Val Met Ser His His Val Pro Pro			
64	225	230	235	240
65	atg gaa gat tgt aag gaa caa gag cct atc atg gac aac aat att tct	768		
66	Met Glu Asp Cys Lys Glu Gln Glu Pro Ile Met Asp Asn Asn Ile Ser			
67	245	250	255	
68	ctg gtg cct ttt gag aga cct gct gtc ata gag aag ctc acg gca aat	816		
69	Leu Val Pro Phe Glu Arg Pro Ala Val Ile Glu Lys Leu Thr Ala Asn			
70	260	265	270	
71	atg gga aag cgc aaa agc tcc act cct cag aag ttt gtg ggg gaa aag	864		
72	Met Gly Lys Arg Lys Ser Ser Thr Pro Gln Lys Phe Val Gly Glu Lys			
73	275	280	285	
74	ctt atg cga ttc agc tac cca gat att cat ttt gat atg aac tta aca	912		
75	Leu Met Arg Phe Ser Tyr Pro Asp Ile His Phe Asp Met Asn Leu Thr			
76	290	295	300	
77	tat gag aag gag gct gag ctg atg cag tct cat atg atg gac caa gcc	960		
78	Tyr Glu Lys Glu Ala Glu Leu Met Gln Ser His Met Met Asp Gln Ala			
79	305	310	315	320
80	atc aac aat gca atc acc tac ctt gga gct gag gcc ctt cac cct ctg	1008		
81	Ile Asn Asn Ala Ile Thr Tyr Leu Gly Ala Glu Ala Leu His Pro Leu			
82	325	330	335	
83	atg cag cat gca cca agc aca atc gct gag gtg gcc cca gtt ata agc	1056		
84	Met Gln His Ala Pro Ser Thr Ile Ala Glu Val Ala Pro Val Ile Ser			
85	340	345	350	
86	tca gct tat tct cag gtc tat cat cca aac agg ata gaa aga ccc att	1104		
87	Ser Ala Tyr Ser Gln Val Tyr His Pro Asn Arg Ile Glu Arg Pro Ile			
88	355	360	365	
89	agc agg gaa aca tct gat agt cac gaa aac aac atg gat ggc ccc atc	1152		
90	Ser Arg Glu Thr Ser Asp Ser His Glu Asn Asn Met Asp Gly Pro Ile			
91	370	375	380	
92	tct ctc atc aga cca aag agt cga ccc cag gaa aga gag gcc tcg ccc	1200		
93	Ser Leu Ile Arg Pro Lys Ser Arg Pro Gln Glu Arg Glu Ala Ser Pro			
94	385	390	395	400

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95	agc aat agc tgc ctc gat tct act gac tca gaa agt agc cat gat gac	1248
96	Ser Asn Ser Cys Leu Asp Ser Thr Asp Ser Glu Ser Ser His Asp Asp	
97	405 410 415	
98	cgc cag tcc tac caa gga aac cct gcc tta aat ccc aag agg aaa caa	1296
99	Arg Gln Ser Tyr Gln Gly Asn Pro Ala Leu Asn Pro Lys Arg Lys Gln	
100	420 425 430	
101	agc cca gct tac atg aag gag gat gtc aag gct ttg gat gct acc aag	1344
102	Ser Pro Ala Tyr Met Lys Glu Asp Val Lys Ala Leu Asp Ala Thr Lys	
103	435 440 445	
104	gcc ccc aag ggc tct ctg aag gac atc tat aag gtt ttc aat gga gaa	1392
105	Ala Pro Lys Gly Ser Leu Lys Asp Ile Tyr Lys Val Phe Asn Gly Glu	
106	450 455 460	
107	gga gaa cag ata agg gcc ttc aag tgt gag cac tgc cga gtc ctt ttt	1440
108	Gly Glu Gln Ile Arg Ala Phe Lys Cys Glu His Cys Arg Val Leu Phe	
109	465 470 475 480	
110	cta gac cat gtc atg tac acc att cac atg ggt tgc cat ggc tac cgg	1488
111	Leu Asp His Val Met Tyr Thr Ile His Met Gly Cys His Gly Tyr Arg	
112	485 490 495	
113	gac cca ctg gaa tgc aac atc tgt ggc tac aga agc cag gac cgc tac	1536
114	Asp Pro Leu Glu Cys Asn Ile Cys Gly Tyr Arg Ser Gln Asp Arg Tyr	
115	500 505 510	
116	gaa ttt tca tca cac att gtt ggg ggg cag cac aca ttc cac	1578
117	Glu Phe Ser Ser His Ile Val Gly Gly Gln His Thr Phe His	
118	515 520 525	
119	taggcgttgc cattccaagg	1598
120	<210> SEQ ID NO 2	
121	<211> LENGTH: 526	
122	<212> TYPE: PRT	
123	<213> ORGANISM: Mus musculus	
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127	Ser Pro Glu Gly Glu His Ala Asn Met Ala Ile Asp Leu Thr Ser Ser	
128	20 25 30	
129	Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asn	
130	35 40 45	
131	Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Gln Pro	
132	50 55 60	
133	Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser Ser Leu	
134	65 70 75 80	
135	Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg Lys Val	
136	85 90 95	
137	Gln Asp Leu Gln Gly Glu Gly Ile Arg Leu Pro Asn Gly Lys Leu	
138	100 105 110	
139	Lys Cys Asp Val Cys Gly Met Val Cys Ile Gly Pro Asn Val Leu Met	
140	115 120 125	
141	Val His Lys Arg Ser His Thr Gly Glu Arg Pro Phe His Cys Asn Gln	
142	130 135 140	
143	Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys	
144	145 150 155 160	

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145 Leu His Ser Gly Glu Lys Pro Phe Lys Cys Pro Phe Cys Ser Tyr Ala
146 165 170 175
147 Cys Arg Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val
148 180 185 190
149 Gly Lys Pro His Lys Cys Asn Tyr Cys Gly Arg Ser Tyr Lys Gln Arg
150 195 200 205
151 Thr Ser Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Gln Asn
152 210 215 220
153 Val Ser Met Glu Ala Ala Gly Gln Val Met Ser His His Val Pro Pro
154 225 230 235 240
155 Met Glu Asp Cys Lys Glu Gln Glu Pro Ile Met Asp Asn Asn Ile Ser
156 245 250 255
157 Leu Val Pro Phe Glu Arg Pro Ala Val Ile Glu Lys Leu Thr Ala Asn
158 260 265 270
159 Met Gly Lys Arg Lys Ser Ser Thr Pro Gln Lys Phe Val Gly Glu Lys
160 275 280 285
161 Leu Met Arg Phe Ser Tyr Pro Asp Ile His Phe Asp Met Asn Leu Thr
162 290 295 300
163 Tyr Glu Lys Glu Ala Glu Leu Met Gln Ser His Met Met Asp Gln Ala
164 305 310 315 320
165 Ile Asn Asn Ala Ile Thr Tyr Leu Gly Ala Glu Ala Leu His Pro Leu
166 325 330 335
167 Met Gln His Ala Pro Ser Thr Ile Ala Glu Val Ala Pro Val Ile Ser
168 340 345 350
169 Ser Ala Tyr Ser Gln Val Tyr His Pro Asn Arg Ile Glu Arg Pro Ile
170 355 360 365
171 Ser Arg Glu Thr Ser Asp Ser His Glu Asn Asn Met Asp Gly Pro Ile
172 370 375 380
173 Ser Leu Ile Arg Pro Lys Ser Arg Pro Gln Glu Arg Glu Ala Ser Pro
174 385 390 395 400
175 Ser Asn Ser Cys Leu Asp Ser Thr Asp Ser Glu Ser Ser His Asp Asp
176 405 410 415
177 Arg Gln Ser Tyr Gln Gly Asn Pro Ala Leu Asn Pro Lys Arg Lys Gln
178 420 425 430
179 Ser Pro Ala Tyr Met Lys Glu Asp Val Lys Ala Leu Asp Ala Thr Lys
180 435 440 445
181 Ala Pro Lys Gly Ser Leu Lys Asp Ile Tyr Lys Val Phe Asn Gly Glu
182 450 455 460
183 Gly Glu Gln Ile Arg Ala Phe Lys Cys Glu His Cys Arg Val Leu Phe
184 465 470 475 480
185 Leu Asp His Val Met Tyr Thr Ile His Met Gly Cys His Gly Tyr Arg
186 485 490 495
187 Asp Pro Leu Glu Cys Asn Ile Cys Gly Tyr Arg Ser Gln Asp Arg Tyr
188 500 505 510
189 Glu Phe Ser Ser His Ile Val Gly Gly Gln His Thr Phe His
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191 <210> SEQ ID NO 3
192 <211> LENGTH: 1520
193 <212> TYPE: DNA
194 <213> ORGANISM: Mus musculus

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195 <220> FEATURE:
 196 <221> NAME/KEY: CDS
 197 <222> LOCATION: (1)...(1500)
 198 <400> SEQUENCE: 3

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201	1 5 10 15	
202	tca ccc gaa ggg gaa cac gcc aat atg gcc att gac ctc acc tca agc	96
203	Ser Pro Glu Gly Glu His Ala Asn Met Ala Ile Asp Leu Thr Ser Ser	
204	20 25 30	
205	acg ccc aat gga cag cac gcc tcg cca agt cac atg aca agc aca aat	144
206	Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asn	
207	35 40 45	
208	tct gta aag ctg gaa atg cag agt gat gaa gag tgt gac agg cag ccc	192
209	Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Gln Pro	
210	50 55 60	
211	ctg agc cgt gag gat gag atc agg ggc cac gat gag ggg agc agc cta	240
212	Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser Ser Leu	
213	65 70 75 80	
214	gaa gaa ccc cta att gag agc agc gag gtg gcc gac aac agg aaa gtc	288
215	Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg Lys Val	
216	85 90 95	
217	cag gac ctt caa ggc gag gga atc cgg ctt ccg aat ggt gag cgg	336
218	Gln Asp Leu Gln Gly Glu Gly Ile Arg Leu Pro Asn Gly Glu Arg	
219	100 105 110	
220	ccc ttc cac tgt aac cag tgc gga gct tct ttt acc cag aag ggc aac	384
221	Pro Phe His Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn	
222	115 120 125	
223	ctt ctg aga cac ata aag tta cac tct gga gag aag ccc ttc aaa tgt	432
224	Leu Leu Arg His Ile Lys Leu His Ser Gly Glu Lys Pro Phe Lys Cys	
225	130 135 140	
226	cct ttc tgt agc tat gct tgt aga aga agg gac gct ctc aca gga cac	480
227	Pro Phe Cys Ser Tyr Ala Cys Arg Arg Asp Ala Leu Thr Gly His	
228	145 150 155 160	
229	ctc agg acc cat tct gtg ggt aaa cct cac aag tgt aac tac tgt ggc	528
230	Leu Arg Thr His Ser Val Gly Lys Pro His Lys Cys Asn Tyr Cys Gly	
231	165 170 175	
232	cga agc tac aag cag cgc acg tca ctg gag gaa cac aag gaa cgc tgt	576
233	Arg Ser Tyr Lys Gln Arg Thr Ser Leu Glu Glu His Lys Glu Arg Cys	
234	180 185 190	
235	cac aac tat ctc cag aat gtc agc atg gag gct gcc ggg cag gtc atg	624
236	His Asn Tyr Leu Gln Asn Val Ser Met Glu Ala Ala Gly Gln Val Met	
237	195 200 205	
238	agt cac cat gta ccg cct atg gaa gat tgt aag gaa caa gag cct atc	672
239	Ser His His Val Pro Pro Met Glu Asp Cys Lys Glu Gln Glu Pro Ile	
240	210 215 220	
241	atg gac aac aat att tct ctg gtg cct ttt gag aga cct gct gtc ata	720
242	Met Asp Asn Asn Ile Ser Leu Val Pro Phe Glu Arg Pro Ala Val Ile	
243	225 230 235 240	
244	gag aag ctc acg gca aat atg gga aag cgc aaa agc tcc act cct cag	768

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
